

SEQUENCE LISTING

<110> ImClone Systems, Inc.
Liu, Meilin
Zhu, Zhenping

<120> Human Anti-Epidermal Growth Factor Receptor Antibody

<130> 11245/51076

<140> not assigned

<141> 2005-03-21

<150> US 60/554,555

<151> 2004-03-19

<150> US 60/624,264

<151> 2004-11-02

<160> 25

<170> PatentIn version 3.3

<210> 1

<211> 24

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (24)

<400> 1

agc agt ggt gat tac tac tgg agt
Ser Ser Gly Asp Tyr Tyr Trp Ser
1 5

24

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<211> 8

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<213> Homo sapiens

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Ser Ser Gly Asp Tyr Tyr Trp Ser
1 5

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<213> Homo sapiens

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tac atc tat tac agt ggg agc acc gac tac aac ccg tcc ctc aag agt 48
 Tyr Ile Tyr Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

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Tyr Ile Tyr Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys Ser
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 gtg tcg att ttt gga gtg ggg aca ttt gac tac 33
 Val Ser Ile Phe Gly Val Gly Thr Phe Asp Tyr
 1 5 10

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<400> 6

Val Ser Ile Phe Gly Val Gly Thr Phe Asp Tyr
 1 5 10

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 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt 96
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
 20 25 30

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gat tac tac tgg agt tgg atc cgc cag ccc cca ggg aag ggc ctg gag      144
Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
      35                      40                      45

tgg att ggg tac atc tat tac agt ggg agc acc gac tac aac ccg tcc      192
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
      50                      55                      60

ctc aag agt cga gtc acc atg tcc gta gac acg tcc aag aat cag ttt      240
Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
      65                      70                      75                      80

tcc ctg aag gtc aac tct gtg acc gcc gca gac acg gct gtg tat tac      288
Ser Leu Lys Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
      85                      90                      95

tgt gcg aga gtg tcg att ttt gga gtg ggg aca ttt gac tac tgg ggc      336
Cys Ala Arg Val Ser Ile Phe Gly Val Gly Thr Phe Asp Tyr Trp Gly
      100                     105                     110

cag ggc acc ctg gtc acc gtc tca agc      363
Gln Gly Thr Leu Val Thr Val Ser Ser
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<210> 8
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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
      20                      25                      30

Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
      35                      40                      45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
      50                      55                      60

Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65                      70                      75                      80

Ser Leu Lys Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
      85                      90                      95

Cys Ala Arg Val Ser Ile Phe Gly Val Gly Thr Phe Asp Tyr Trp Gly
      100                     105                     110

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Gln Gly Thr Leu Val Thr Val Ser Ser
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Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu
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30

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Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu
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Asp Ala Ser Asn Arg Ala Thr
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21

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Asp Ala Ser Asn Arg Ala Thr
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<210> 13
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 His Gln Tyr Gly Ser Thr Pro Leu
 1 5

24

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 Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc tac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctc ctc atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

gaa gat ttt gca gtg tat tac tgt cac cag tat ggt agc aca cct ctc 288
 Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr Gly Ser Thr Pro Leu
 85 90 95

act ttc ggc gga ggg acc aag gcg gag atc aaa 321
 Thr Phe Gly Gly Gly Thr Lys Ala Glu Ile Lys

100

105

<210> 16
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Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr Gly Ser Thr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Ala Glu Ile Lys
 100 105

<210> 17
 <211> 15
 <212> PRT
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<400> 17

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<210> 18
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<400> 18

Gly Gly Gly Gly Ser
 1 5

<210> 19

<211> 10
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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 20
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<400> 20
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<210> 21
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cgagctagcg cttgagacgg tgaccagggt g 31

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val His Ser